

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 15:32:02 ; Search time 26 Seconds
(without alignments)
3701.175 Million cell updates/sec

Title: US-10-046-433-40
Perfect score: 1001
Sequence: 1 MAEPGSHHLSARVRGTER.....LGRSHLPRLGLMDLQCR 1001

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

word size : 0

Total number of hits satisfying chosen parameters: 283224

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Listing first 150 summaries

Database : PIR_73:★

```

1: pir2:1
2: pir2:1
3: pir3:1
4: pir4:1

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	8	0.8	133	2	D48776	polyprotein (32/NS
2	8	0.8	284	2	A69536	mevalonate kinase
3	8	0.8	353	1	OEPRHC	peroxidase (EC 1.1
4	8	0.8	353	2	S37495	peroxidase (EC 1.1
5	8	0.8	353	2	T6118	peroxidase - Arabi
6	8	0.8	354	2	JU0457	peroxidase (EC 1.1
7	8	0.8	443	2	A71686	colb protein precu
8	8	0.8	444	2	F97750	colb protein precu
9	8	0.8	695	2	F72075	hypothetical prote
10	8	0.8	695	2	F86547	hypothetical prote
11	8	0.8	695	2	F81592	hypothetical prote
12	8	0.8	744	2	T39841	topoisomerase II as
13	7	0.7	73	1	DNBPD8	DNA-binding protei
14	7	0.7	75	2	T38534	small nuclear ribo
15	7	0.7	91	2	G84870	hypothetical prote
16	7	0.7	91	2	T47805	u6 snRNA-associate
17	7	0.7	100	1	B43719	urasea (EC 3.5.1.5
18	7	0.7	100	1	S08478	urasea (EC 3.5.1.5
19	7	0.7	106	2	B47050	urasea (EC 3.5.1.5
20	7	0.7	106	2	C95075	hypothetical prote
21	7	0.7	116	2	T47435	hypothetical prote
22	7	0.7	124	2	T24876	hypothetical prote
23	7	0.7	134	2	C90490	conserved hypotet
24	7	0.7	159	2	H84424	hypothetical prote
25	7	0.7	175	2	F97734	formylmethionine d
26	7	0.7	175	2	E64366	hypothetical prote
27	7	0.7	181	2	S78336	conserved hypotet
28	7	0.7	197	2	F75498	conserved hypotet
29	7	0.7	215	2	A00056	probable phosphogl

[illegible]

QY	132	HGFASLSA	139	Best Local Similarity	100.0%	Pred. No. 5:
				Matches	8;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	26	HGFASLSA	33			
RESULT 2						
	A69536	malonate kinase (mvk) homolog - Archaeoglobus fulgidus				
	CjSpecies:	Archaeoglobus fulgidus				
	CjDate:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000				
	CjAccession:	A69536				
	RjKlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.					
	AjAuthors:	Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.				
	AjTitle:	The complete genome sequence of the hyperthermophilic, sulfate-reducing archae				
	AjReference number:	A69250; PMID:98049343; PMID:9389475				
	AjAccession:	A69536				
	AjStatus:	preliminary; nucleic acid sequence not shown; translation not shown				
	AjMolecule type:	DNA				
	AjResidues:	1-284 <RLF>				
	AjCross-references:	GB:AE000946; GB:AE000782; NID:G2689269; PIDN:AAB88965.1; PID:G264823				
Query Match						
	Best Local Similarity	0.8%; Score 8; DB 2; Length 284;				
	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	593	LEASDVS	600			
DB	201	LEASDVS	208			
RESULT 3						
	OPRHC	peroxidase (EC 1.11.1.7) CIA precursor - horseradish				
	CjSpecies:	Armoracia rusticana (horseradish)				
	CjDate:	24-Apr-1984 #sequence_revision 12-Apr-1996 #ext_change 01-Dec-2000				
	CjAccession:	S00625; S32972; A00502; PC7025				
	RjFujiyama, K.; Takemura, H.; Shibayama, S.; Kobayashi, K.; Choi, J.K.; Shimmyo, A.; Tak					
	Eur, J.	Biochem. 173, 661-687, 1988				
	AjTitle:	Structure of the horseradish peroxidase isozyme C genes.				
	AjReference number:	S00625; PMID:88225087; PMID:3371152				
	AjAccession:	S00625				

A; Residu

Eur. J. Biochem. 96, 483-502, 1979
 A:/Title: Amino acid sequence studies of horseradish peroxidase. Amino and carboxyl termi
 radish peroxidase C.
 A:/Reference number: S32972; NCID:79236311; PMID:28113
 A:/Accession: S32972
 A:/Molecule type: protein
 A:/Residues: 31-338 <WE1>
 R:/Weilinder, K.G.
 FEBS Lett. 72, 19-23, 1976
 A:/Title: Covalent structure of the glycoprotein horseradish peroxidase (EC 1.11.1.7).
 A:/Reference number: A00502; NCID:77068850; PMID:1001465
 A:/Accession: A00502
 A:/Molecule type: protein
 A:/Residues: 31-338 <WE2>
 R:/Gazaryan, I.G.; Chubur, T.A.; Ignatenko, O.V.; Mareeva, E.A.; Orlova, M.A.; Kapelush,
 Biochem. Biophys. Res. Commun. 262, 297-301, 1999
 A:/Title: Tryptophanless recombinant horseradish peroxidase: Stability and catalytic prop
 A:/Reference number: PC7025; NCID:99382281; PMID:1048108
 A:/Accession: PC7025
 A:/Molecule type: DNA
 A:/Residues: 31-338 <GA2>

C:Genetics: prxC1; w117E
 C:Superfamily: peroxidase
 C:Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase; pyr
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31/38/Product: peroxidase C1 #status experimental <MAT>
 F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F:41-121,74-79,127-231,207-239/Disulfide bonds: #status experimental
 F:43,87,188,216,228,244,285,298/Binding site: carbohydrate (Asn) (covalent) #status exp
 F:68/Active site: Arg #status predicted
 F:72,200/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 0.8%; Score 8; DB 1; Length 353;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLAGPS 687
 |||||
 Db 139 VTLAGPS 146

RESULT 4

S37495
 Peroxidase (EC 1.11.1.7) Cb - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
 C:Accession: S37495
 R:Intapuk, C.; Takano, M.; Shimmyo, A.
 submitted to the EMBL Data Library, April 1993
 A:Description: Nucleotide sequence of a new cDNA for peroxidase from Arabidopsis thalian
 A:Reference number: S37495
 A:Accession: S37495
 A:Molecule type: mRNA
 A:Residues: 1-353 <INT>
 A:Cross-references: EMBL:X71794; NID:9405610; PIDN:CAA50677.1; PID:9405611
 C:Genetics:
 A:Gene: prxCb
 C:Superfamily: peroxidase
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
 F:41-121/Disulfide bonds: #status predicted
 F:68/Active site: Arg #status predicted
 F:72,200/Binding site: heme iron (His) (axial ligands) #status predicted
 F:74-79/Disulfide bonds: #status predicted
 F:127-231/Disulfide bonds: #status predicted
 F:207-239/Disulfide bonds: #status predicted

Query Match 0.8%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLAGPS 687
 |||||
 Db 139 VTLAGPS 146

RESULT 5

T46118
 Peroxidase - Arabidopsis thaliana
 N:Alternate names: protein T2J13.40
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T46118
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, K
 submitted to the Protein Sequence Database, November 1999
 A:Reference number: Z23023
 A:Accession: T46118
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-353 <RIE>
 A:Cross-references: EMBL:AL132967
 A:Experimental source: cultivar Columbia; BAC clone T2J13
 C:Genetics:
 A:Map position: 3

A:Introns: 77/3; 141/3; 198/1
 A:Note: T2J13.40
 C:Superfamily: peroxidase

Query Match 0.8%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLAGPS 687
 |||||
 Db 139 VTLAGPS 146

RESULT 6

JU0457
 Peroxidase (EC 1.11.1.7) C - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 04-Mar-2000
 C:Accession: JU0457; T46119
 R:Intapuk, C.; Higashimura, N.; Yamamoto, K.; Okada, N.; Shimmyo, A.; Takano, M.
 Gene 98, 237-241, 1991
 A:Title: Nucleotide sequences of two genomic DNAs encoding peroxidase of Arabidopsis the
 A:Reference number: JU0457; MUID:9120671; PMID:2016063
 A:Accession: JU0457
 A:Molecule type: DNA
 A:Residues: 1-354 <INT>
 A:Cross-references: GB:MS8380; NID:9166826; PIDN:AAA32849.1; PID:9166827
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, K
 submitted to the Protein Sequence Database, November 1999
 A:Reference number: Z23023
 A:Accession: T46119
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <RIE>
 A:Cross-references: EMBL:AL132967
 A:Experimental source: cultivar Columbia; BAC clone T2J13
 C:Genetics:
 A:Gene: prxCa; T2J13.50
 A:Map position: 3
 A:Introns: 78/3; 142/3; 199/1
 C:Superfamily: peroxidase
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
 F:42-122/Disulfide bonds: #status predicted
 F:69/Active site: Arg #status predicted
 F:73,201/Binding site: heme iron (His) (axial ligands) #status predicted
 F:75-80/Disulfide bonds: #status predicted
 F:128-332/Disulfide bonds: #status predicted
 F:208-240/Disulfide bonds: #status predicted

Query Match 0.8%; Score 8; DB 2; Length 354;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLAGPS 687
 |||||
 Db 140 VTLAGPS 147

RESULT 7

A71686
 ToD protein precursor (ToD) RP302 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: A71686
 R:Andersson, S.G.B.; Zomrodipour, A.; Andersson, J.O.; Sichertz-Ponten, T.; Alsmark, U
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: A71686
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-443 <AND>
 A:Cross-references: GB:AJ235271; GB:AJ235269; NID:93868717; PIDN:CAA14763.1; PID:9386808

A:Experimental source: strain Madrid E
C:Gene: colB, RP302

Query Match 0.8%; Score 8; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 PRGDYIAF 168
DB 340 PRGDYIAF 347

RESULT 8

colB protein precursor [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001

C:Accession: F97750
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia conorii

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: F97750
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL02944.1; PID:G15619474; GSPDB:GN00173
C:Gene: colB

Query Match 0.8%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 PRGDYIAF 168
DB 341 PRGDYIAF 348

RESULT 9

hypothetical protein - Chlamydia pneumoniae (strain CWL029)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000

C:Accession: E72075
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: E72075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-695 <ARN>
A:Cross-references: GB:AE001630; GB:AE001363; NID:94376740; PIDN:AAD18600.1; PID:9437674
A:Experimental source: strain CWL029
C:Gene: CP0458

C:Superfamily: Chlamydia hypothetical protein CP0462

Query Match 0.8%; Score 8; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 VSSCVAGI 875
DB 67 VSSCVAGI 74

RESULT 10

hypothetical protein CP0458 [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: F86547
R:Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise

Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10873362

A:Accession: F86547
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-695 <STO>
A:Cross-references: GB:BA000008; NID:98978828; PIDN:BA98664.1; GSPDB:GN00142

A:Experimental source: strain J138
C:Gene: CP10458

C:Superfamily: Chlamydia hypothetical protein CP0462

Query Match 0.8%; Score 8; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 VSSCVAGI 875
DB 67 VSSCVAGI 74

RESULT 11

hypothetical protein CP0294 [imported] - Chlamydia pneumoniae (strain AR39)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000

C:Accession: F81592
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwim, M.; Neilson, W.; Deboy, R.; Kolony, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: F81592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-695 <REA>
A:Cross-references: GB:AE002191; GB:AE002161; NID:97189216; PIDN:AAF38151.1; PID:9718922
A:Experimental source: strain AR39, HL cells
C:Gene: CP0294

C:Superfamily: Chlamydia hypothetical protein CP0462

Query Match 0.8%; Score 8; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 VSSCVAGI 875
DB 67 VSSCVAGI 74

RESULT 12

topoisomerase II associated protein pat1 homolog - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999

C:Accession: T39841
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davlin, K.; Churcher, C.M. submitted to the EMBL Data Library, February 1998

A:Reference number: Z21884
A:Accession: T39841
A:Status: preliminary; translated from GB/EMBL/DD8J

A:Molecule type: DNA
A:Residues: 1-744 <LYN>

A:Cross-references: EMBL:AL021839; PIDN:CAA17064.1; GSPDB:GN00067; SPDB:SPBC1967.10C
A:Experimental source: strain 972h-; cosmid c19G7
C:Gene: SPDB:SPBC1967.10C
A:Map position: 2

A;introns: 26/2; 60/1; 656/2; 713/2

Query Match 0.8%; Score 8; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LKQSGTVA 190
|||||
DB 642 LKQSGTVA 649

RESULT 13

DNA-Binding protein Ner - phage D108

C;Species: phage D108
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: A24680; S07931
R;Tollas, P.P.; Dubow, M.S.
EMBO J. 4, 3031-3037, 1985.
A;Title: The cloning and characterization of the bacteriophage D108 regulatory DNA-binding protein.
A;Reference number: A24680; MUID:86055744; PMID:2998774
A;Accession: A24680
A;Molecule type: DNA
A;Residues: 1-73 <TO>

A;Cross-references: GB:M26291; NID:g16194; PID:AAA32206.1; PID:g16195
R;Mizunuchi, M.; Weisberg, R.A.; Mizunuchi, K.
Nucleic Acids Res. 14, 3813-3825, 1986
A;Title: DNA sequence of the control region of phage D108: the N-terminal amino acid sequence.
A;Reference number: S07370; MUID:86232621; PMID:3012481
A;Accession: S07931
A;Molecule type: DNA
A;Residues: 1-73 <MIT>

A;Cross-references: EMBL:X03847; NID:g15439; PID:CAA27475.1; PID:g15441
C;Genetics:
A;Gene: ner
C;Superfamily: phage D108 DNA-binding protein
C;Keywords: DNA binding

Query Match 0.7%; Score 7; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 982 IGRSNHL 988
|||||
DB 31 IGRSNHL 37

RESULT 14

small nuclear ribonucleoprotein, F-like - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: J38534
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21748
A;Accession: J38534

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-75 <OLI>
A;Cross-references: EMBL:Z99165; PIDN:CA854975.1; GSPDB:GN00066; SPDB:SPAC2F3.17C
A;Experimental source: strain 972h-; cosmid c2F3
C;Genetics:
A;Gene: SPDB:SPAC2F3.17C
A;Map position: 1
A;introns: 29/1; 67/1

Query Match 0.7%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
|||||

DB 63 RGNVLY 69

RESULT 15

hypothetical protein At2g43810 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84870
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84870
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>

A;Cross-references: GB:A8002093; NID:g2281089; PIDN:AA64025.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g43810
A;Map position: 2

Query Match 0.7%; Score 7; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
|||||
DB 73 RGNVLY 79

RESULT 16

T47805

U6 snRNA-associated Sm-like protein - Arabidopsis thaliana

N;Alternate names: protein F24G16.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47805
R;P'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24477
A;Accession: T47805

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <DAN>
A;Cross-references: EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
C;Genetics:
A;Map position: 3
A;introns: 39/1; 77/1
A;Note: F24G16.80

Query Match 0.7%; Score 7; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
|||||
DB 73 RGNVLY 79

RESULT 17

B43719

urease (EC 3.5.1.5) 11K chain - Proteus mirabilis

N;Alternate names: urease gamma chain
C;Species: Proteus mirabilis
C;Date: 03-Mar-1993 #sequence_revision 02-Dec-1994 #text_change 18-Jun-1999
C;Accession: B43719
R;Jones, B.D.; Mobley, H.L.T.
J. Bacteriol. 171, 6414-6422, 1989
A;Title: Proteus mirabilis urease: nucleotide sequence determination and comparison with

A:Reference number: A43719; MUID:90078080; PMID:2687233
A:Accession: B43719
A:Molecule type: DNA
A:Residues: 1-100 <JUN>
A:Cross-references: GB:M1834; NID:g150914; PIDN:AAA25667.1; PID:g150916
C:Genetics:
A:Gene: urea
C:Function:
A:Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two
C:Superfamily: urease 11K chain; urease 11K chain homology
C:Keywords: heterotrimer; hydrolase; metalloprotein
F:1-100/Domain: urease 11K chain homology <U11>

Query Match 0.7%; Score 7; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 960 SCAIMEG 966
DB 40 SCAIMEG 46

RESULT 18
S08478
urease (EC 3.5.1.5) 11K chain - Proteus vulgaris
N:Alternate names: urease gamma chain
C:Species: Proteus vulgaris
C>Date: 29-Jan-1993 #sequence_revision 02-Dec-1994 #text_change 20-Apr-2001
C:Accession: S08478
R:Moersdorf, G.; Kaltwasser, H.
FEMS Microbiol. Lett. 66, 67-74, 1991
A:Title: Cloning of the genes encoding urease from Proteus vulgaris and sequencing of th
A:Reference number: S08478; MUID:92038908; PMID:1936338
A:Accession: S08478
A:Molecule type: DNA
A:Residues: 1-100 <MOE>
A:Cross-references: EMBL:X51816; NID:g45933; PIDN:CAA36113.1; PID:g45934
C:Genetics:
A:Gene: urea
C:Function:
A:Description: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
C:Superfamily: urease 11K chain; urease 11K chain homology
C:Keywords: heterotrimer; hydrolase; metalloprotein
F:1-100/Domain: urease 11K chain homology <U11>

Query Match 0.7%; Score 7; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 960 SCAIMEG 966
DB 40 SCAIMEG 46

RESULT 19
B47090
urease (EC 3.5.1.5) chain A - Escherichia coli
C:Species: Escherichia coli
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C:Accession: B47090
R:D'Orazio, S.E.; Collins, C.M.
J. Bacteriol. 175, 1860-1864, 1993
A:Title: Characterization of a plasmid-encoded urease gene cluster found in members of t
A:Reference number: A47090; MUID:93194816; PMID:8443894
A:Accession: B47090
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-100 <DIO>
A:Cross-references: GB:I03307; NID:g148150; PIDN:AAA24445.1; PID:g148152
A:Note: sequence extracted from NCBI backbone (NCBIN:127840, NCBI:P:127842)
C:Genetics:

A:Gene: Urea
C:Superfamily: urease 11K chain; urease 11K chain homology
C:Keywords: hydrolase
F:1-100/Domain: urease 11K chain homology <U11>

Query Match 0.7%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 960 SCAIMEG 966
DB 40 SCAIMEG 46

RESULT 20
C95075
hypothetical protein SP0650 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: C95075
R:Rettlein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KIR>
A:Cross-references: GB:AB005672; PIDN:AMK74796.1; PID:g14972123; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0650

Query Match 0.7%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 MILTLV 476
DB 1 MILTLV 7

RESULT 21
T47435
hypothetical protein T22K7.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
C:Accession: T47435
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T47435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-116 <RIE>
A:Cross-references: EMBL:AL138641
A:Experimental source: cultivar Columbia; BAC clone T22K7
C:Genetics:
A:Map position: 3
A:Note: T22K7.130
C:Superfamily: Arabidopsis thaliana hypothetical protein T22K7.130

Query Match 0.7%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 ETTVLSG 440
DB 34 ETTVLSG 40

RESULT 22

T24876

hypothetical protein T13F2.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2000

C:Accession: T24876

R:Swindburne, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19947

A:Accession: T24876

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-124 <WIL>

A:Cross-references: EMBL:Z81122; PIDN:CAH03353.1; GSPDB:GN00022; CESP:T13F2.2

A:Experimental source: clone T13F2

C:Genetics:

A:Gene: CESP:T13F2.2

A:Map position: 4

A:Initons: 27/3; 61/3; 91/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein T13F2.2

Query Match

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 YYIDRDS 615

DB 87 YYIDRDS 93

RESULT 23

C90490

conserved hypothetical protein [imported] - *Sulfolobus solfataricus*C:Species: *Sulfolobus solfataricus*

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: C90490

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.

arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: C90490

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <KUR>

A:Cross-references: GB:AE006641; NID:G13816489; PIDN:AAK43178.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO3078

Query Match

Best Local Similarity 100.0%; Pred. No. 58;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTDNVT 720

DB 76 CTDNVT 82

RESULT 24

H84224

hypothetical protein Vng0670h [imported] - *Halobacterium* sp. NRC-1C:Species: *Halobacterium* sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: H84224

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Leaky, S.

; Lettner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of *Halobacterium* species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016550

A:Accession: H84224
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-159 <STO>
 A:Cross-references: GB:AE004437; NID:G10580256; PIDN:AAG19164.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG0670H

Query Match

Best Local Similarity 100.0%; Pred. No. 66;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LLMAGT 34

DB 124 LLMAGT 130

RESULT 25

P97734

formylmethionine deformylase (EC 3.5.1.31) - *Rickettsia conorii* (strain Malish 7)C:Species: *Rickettsia conorii*

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: P97734

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barde, V.; Samson, D.; Ro

science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: P97734

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <KUR>

A:Cross-references: GB:AE006914; PIDN:AL02816.1; PID:G15619334; GSPDB:GN00173

C:Genetics:

A:Gene: defl

A:Superfamily: polypeptide deformylase

C:Keywords: hydrolase

Query Match

Best Local Similarity 100.0%; Pred. No. 72;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 ISLPEOR 898

DB 100 ISLPEOR 106

RESULT 26

E64396

hypothetical protein MJ0773 - *Methanococcus jannaschii*C:Species: *Methanococcus jannaschii*

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: E64396

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reich, C.T.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.

; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Huret, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: E64396

A:Status: preliminary

A:Molecule type: nucleic acid sequence not shown; translation not shown

A:Residues: 1-175 <BDU>

A:Cross-references: GB:U67522; GB:U77117; NID:G2826315; PIDN:AA898777.1; PID:G1499593; T

C:Genetics:

A:Map position: REV94542-694015

C:Superfamily: *Methanococcus jannaschii* hypothetical protein MJ0773

Query Match

Best Local Similarity 100.0%; Pred. No. 72;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 687 SFTSKL 693

Db 68 SFTSKGL 74

RESULT 27

S78336

Conserved hypothetical protein 181 - *Odontella sinensis* chloroplastC/Species: chloroplast *Odontella sinensis*

C/Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000

C/Accession: S78336

R/Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freiler, U.

Plant Mol. Biol. Rep. 13, 336-342, 1995

A/Title: The Chloroplast Genome of a Chlorophyll a+c-containing Alga, *Odontella sinensis*

A/Reference number: S78338

A/Accession: S78336

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-181 <KOW>

A/Cross-references: EMBL:Z67753; NID:g1185127; PIDN:CAA91709.1; PID:g1185226

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C/Genetics:

A/Gene: ysf4

A/Genome: chloroplast

C/Superfamily: conserved hypothetical protein s110226

C/Keywords: chloroplast

Query Match

Best Local Similarity 0.7%; Score 7; DB 2; Length 181;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 28

F75498

Conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)C/Species: *Deinococcus radiodurans*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C/Accession: F75498

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, H.O.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A/Reference number: A75250; MIMD:20036896; PMID:10567266

A/Accession: F75498

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-197 <WHI>

A/Cross-references: GB:AE001918; GB:AE000513; NID:g6458294; PIDN:AAF10178.1; PID:g645829

C/Genetics:

A/Gene: DR0598

A/Map position: 1

Query Match

Best Local Similarity 0.7%; Score 7; DB 2; Length 197;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IYTAAGA 464

Db 179 IYTAAGA 185

RESULT 29

AD0056

Probable phosphoglycerate mutase (EC 5.4.2.1) [imported] - *Yersinia pestis* (strain CO92)C/Species: *Yersinia pestis*

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C/Accession: AD0056

R/Fairhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MIMD:21470413; PMID:11586360

A/Accession: AD0056

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-215 <KUR>

A/Cross-references: GB:AL590842; PIDN:CAC89311.1; PID:g15978547; GSPDB:GN00175

C/Genetics:

A/Gene: gpmB

C/Superfamily: Aquifex aeolicus phosphoglycerate mutase; phosphoglycerate mutase homolog

C/Keywords: intramolecular transferase; isomerase

Query Match

Best Local Similarity 0.7%; Score 7; DB 2; Length 215;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 RIBEGES 728

Db 115 RIBEGES 121

RESULT 30

A91298

Phosphoglyceromutase 2 [imported] - *Escherichia coli* (strain O157:H7, substrain RIMD 050C/Species: *Escherichia coli*

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001

C/Accession: A91298

R/Hayashi, T.; Makino, K.; Ohishi, M.; Kurukawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Gagawa, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen

A/Reference number: A99629; MIMD:21156231; PMID:11258796

A/Accession: A91298

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-215 <HAY>

A/Cross-references: GB:BA000007; PIDN:BA838776.1; PID:g13364831; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: EGS353

C/Superfamily: Aquifex aeolicus phosphoglycerate mutase; phosphoglycerate mutase homolog

Query Match

Best Local Similarity 0.7%; Score 7; DB 2; Length 215;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 RIBEGES 728

Db 115 RIBEGES 121

RESULT 31

C86139

Phosphoglyceromutase 2 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)C/Species: *Escherichia coli*

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001

C/Accession: C86139

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A/Reference number: AB5480; MIMD:21074935; PMID:11206551

A/Accession: C86139

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-215 <STO>

A/Cross-references: GB:AE005174; NID:g12519424; PIDN:AAG59575.1; GSPDB:GN00145; UNGP:Z59

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: gpmB

C:Superfamily: Aquifex aeolicus phosphoglycerate mutase; phosphoglycerate mutase homolog

Query Match 0.7%; Score 7; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 85;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 RPPGES 728
|||||
DB 115 RPPGES 121

RESULT 32

SS6619

gpmB protein - Escherichia coli (strain K-12)

N:Alternate names: hypothetical protein 0215b

C:Species: Escherichia coli

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002

C/Accession: S56619; B65255

R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 23, 2105-2119, 1995

A>Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.

A/Reference number: S56314; MUID:9534362; PMID:7610040

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-215 <BIR>

A/Cross-references: EMBL:U14003; NID:g1263172; PIND:AAA97291.1; PID:g537235

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perne, N.T.; Burland, V.; Riley, M.; CC

.A.; Rose, D.J.; Mau, B.; Shaoh, Y.

A>Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Accession: B65255

A/Molecule type: DNA

A/Residues: 1-215 <BLAT>

A/Cross-references: GB:AE000509; GB:U00096; NID:g2367383; PIND:AACT7348.1; PID:g1790856;

A/Experimental source: strain K-12, substrain MG1655

C/Genetics:

A:Gene: gpmB

C:Superfamily: Aquifex aeolicus phosphoglycerate mutase; phosphoglycerate mutase homolog

C:Keywords: phosphotidine; phosphoprotein

F:4-185/Domain: phosphoglycerate mutase homology <PGMH>

F:9/Active site: His (phosphotidine intermediate) #struc predicted

Query Match 0.7%; Score 7; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 85;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 RPPGES 728
|||||
DB 115 RPPGES 121

RESULT 33

C71843

Probable uroporphyrinogen-III synthase - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A/Variety: strain J99

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C/Accession: C71843

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Tree, C.; Gibson, R.; Weibers, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A/Reference number: A71800; MUID:99120557; PMID:9923682

A/Accession: C71843

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-223 <ARN>

A/Cross-references: GB:AE001542; GB:AE001439; NID:g4155739; PIND:AA06731.1; PID:g415575

C:Genetics:

A:Gene: hemD

Query Match 0.7%; Score 7; DB 2; Length 223;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 973 LFTSKN 979
|||||
DB 38 LFTSKN 44

RESULT 34

H64672

Uroporphyrinogen III cosynthase - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C/Accession: H64672

R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: H64672

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-226 <TCM>

A/Cross-references: GB:AE000628; GB:AE000511; NID:g2314386; PIND:AA08269.1; PID:g231438

Query Match 0.7%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 973 LFTSKN 979
|||||
DB 38 LFTSKN 44

RESULT 35

UC5966

Transmembrane protein PDHP - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001

C/Accession: UC5966; T40882

R:Iha, H.; Takimoto, M.; Danjoh, I.; Fujiyama, A.

DNA Res. 4, 393-396, 1997

A>Title: Identification and characterization of a novel trans-membrane protein gene, pdh

A/Reference number: UC5966; MUID:98162726; PMID:9501995

A/Accession: UC5966

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: DDBJ:D88384; NID:g2911159; PIND:BAA24946.1; PID:g2911160

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A/Reference number: Z21954

A/Accession: T40882

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-226 <WOO>

A/Cross-references: EMBL:AL031764; PIND:CAA21112.1; GSPDB:GN00068; SPDB:SPCC1235.08c

A/Experimental source: strain 972h-; cosmid c1235

C/Genetics:

A:Gene: SPCC1235.08c

A/Map position: 3

C:Superfamily: Schizosaccharomyces pombe transmembrane protein PDHP

Query Match 0.7%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 ELPHES 789
 |||||
 Db 214 ELPHES 220

RESULT 36

S78180

succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) chain 2 - *Reclinomonas americana* (ATCC N/A) Alternate names: succinate:ubiquinone oxidoreductase

C/Species: mitochondrion *Reclinomonas americana*

A/Variety: ATCC 50394

C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 11-Jun-1999

C/Accession: S78180

R/Name: B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank

Nature 387, 493-497, 1997

A/Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.

A/Reference number: S78127; MUID:97311393; PMID:9168110

A/Accession: S78180

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-239 <LAN>

A/Cross-references: EMBL:AF007261; NID:92258325; PIDN:AAD11913.1; PID:92258379

A/Experimental source: ATCC 50394

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997

C/Genetics:

A/Gene: sdh2

A/Genome: mitochondrion

C/Superfamily: fumarate reductase iron-sulfur protein; ferredoxin 2(4Fe-4S) homology; Fe

C/Keywords: 2Fe-2S; 3Fe-4S; 4Fe-4S; iron-sulfur protein; metalloprotein; mitochondrion;

F/40-82/Domain: ferredoxin (2Fe-2S) homology <FER1>

F/144-226/Domain: ferredoxin 2(4Fe-4S) homology <FER2>

F/61-66,69,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

F/151,154,157,213/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

F/161,208,214/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 0.7%; Score 7; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 WMKTEK 226
 |||||
 Db 123 WMKTEK 129

RESULT 37

T41234

translation initiation factor eIF-6 [imported] - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000

C/Accession: T41234

R/Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 1999

A/Reference number: Z21979

A/Accession: T41234

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-244 <LYN>

A/Cross-references: EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN00068; SPDB:SPCC1919.09

A/Experimental source: strain 972h-; cosmid c1919

C/Genetics:

A/Gene: SPDB:SPCC1919.09

A/Map position: 3

A/Intons: 12/2; 36/2

C/Superfamily: conserved hypothetical protein YP016C

Query Match 0.7%; Score 7; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 SLDPVK 87
 |||||
 Db 87 SLDPVK 93

RESULT 38

T46968

flavoprotein [imported] - *Paracoccus denitrificans* (fragment)

C/Species: *Paracoccus denitrificans*

C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000

C/Accession: T46968

R/Medara, C.; Bardischewsky, F.; Friedrich, C.G.

J. Bacteriol. 179, 5014-5023, 1997

A/Title: Cloning and characterization of sulfite dehydrogenase, two c-type cytochromes, sulfur oxidation.

A/Reference number: Z24324; MUID:97405897; PMID:9260941

A/Accession: T46968

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-247 <MOD>

A/Cross-references: EMBL:X79242; NID:92253074; PIDN:CAA55826.1; PID:92222781

A/Experimental source: strain GB17

C/Genetics:

A/Gene: soxX

Query Match 0.7%; Score 7; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 TVTLAGG 685
 |||||
 Db 114 TVTLAGG 120

RESULT 39

S40006

trypsin (EC 3.4.21.4) precursor - African malaria mosquito

C/Species: *Anopheles gambiae* (African malaria mosquito)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999

C/Accession: S40006

R/Mueller, H.

submitted to the EMBL Data Library, June 1993

A/Reference number: S40003

A/Accession: S40006

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-267 <MUR>

A/Cross-references: EMBL:Z22930; NID:9410323; PIDN:CAA80516.1; PID:9410327

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; protein digestion; serine proteinase

F/42-261/Domain: trypsin homology <TRY>

F/82,127,222/Active site: His, Asp, Ser #status predicted

Query Match 0.7%; Score 7; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AILITVL 926
 |||||
 Db 6 AILITVL 12

RESULT 40

H96009

probable modification methylase protein [imported] - *Sinorhizobium meliloti* (strain 1021)

C/Species: *Sinorhizobium meliloti*

C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C/Accession: H96009

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A/Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: H96009

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-275 <KUR>

A/Cross-references: GB:AL591985; PIDN:CA949744.1; PID:915141231; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSMB
 R:Gallibery, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barley-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C:Accession: AG3112
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woc, I. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.
 C:Date: 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AG3112
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <KUR>
 A:Cross-references: GB:AB008689; PIDN:AA45317.1; PID:G17743007; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4523
 A:Map position: linear chromosome
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 362 EDEGAV 368
 DB 154 EDEGAV 160

RESULT 41
 AG3112
 hypothetical protein Atu4523 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C:Accession: AG3112
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woc, I. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.
 C:Date: 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AG3112
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <KUR>
 A:Cross-references: GB:AB008689; PIDN:AA45317.1; PID:G17743007; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4523
 A:Map position: linear chromosome
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 920 AILLTVL 926
 DB 255 AILLTVL 261

RESULT 42
 AF2179
 hypothetical protein al12989 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AF2179
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Takata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genome Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF2179
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA874688.1; PID:G17132083; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al12989

Query Match 0.7%; Score 7; DB 2; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 752 KAGVSSQ 758
 DB 204 KAGVSSQ 210

RESULT 43
 F98174
 oligopeptide ABC transporter (permease) (AP001508) [imported] - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
 C:Accession: F98174
 R:Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; PMID:11743194
 A:Accession: F98174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-284 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK88920.1; PID:G15158694; GSPDB:GN00170
 A:Genetics:
 A:Gene: AGR L 692
 A:Map position: linear chromosome
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 920 AILLTVL 926
 DB 257 AILLTVL 263

RESULT 44
 A71065
 probable sugar-binding transport system permease protein - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: A71065
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir, M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic eubacterium Pyrococcus horikoshii
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: A71065
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-292 <KAW>
 A:Cross-references: GB:AP000005; MUID:G3236132; PIDN:BA30315.1; PID:G3257632
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1215
 C:Superfamily: inner membrane protein uppa

Query Match 0.7%; Score 7; DB 2; Length 292;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 826 VPGSLIL 832
 DB 79 VPGSLIL 85

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RESULT 45
A87291
succinyl-CoA synthetase, alpha subunit [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C/Accession: A87291
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kollar
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: A87291
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-294 <STO>
A/Cross-references: GB:AE005673; NID:g13421487; PIDN:AAK22325.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC0338
C/Superfamily: succinate-CoA ligase (ADP-forming) alpha chain

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 294;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKVQTE 90
|||||
DB 181 DPKVQTE 187

RESULT 46
T22272
hypothetical protein T01C4.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C/Accession: T22272
R/Graves, T.; Wohlmann, P.
Submitted to the EMBL Data Library, September 1996
A/Description: The sequence of C. elegans cosmid T01C4.
A/Reference number: Z20599
A/Accession: T22272
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-294 <GBA>
A/Cross-references: EMBL:U07858; PIDN:AA09178.1; GSPDB:GN00023; CESP:T01C4.3
A/Experimental source: strain Bristol N2; clone T01C4
C/Genetics:
A/Gene: CESP:T01C4.3
A/Map position: 5
A/Introns: 67/2; 116/2; 142/1; 220/3
C/Superfamily: Caenorhabditis elegans hypothetical protein K07C6.10

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 294;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 FMITLV 475
|||||
DB 39 FMITLV 45

RESULT 47
E97675
succinyl-CoA synthetase alpha chain (AP001515) [imported] - Agrobacterium tumefaciens (S
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C/Accession: E97675
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scant, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

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A/Reference number: A97359; PMID:11743194
A/Accession: E97675
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-300 <KUR>
A/Cross-references: GB:AE007869; PIDN:AAK88358.1; PID:g15157841; GSPDB:GN00169
C/Genetics:
A/Gene: AGR_C_4779
A/Map position: circular chromosome
C/Superfamily: succinate-CoA ligase (ADP-forming) alpha chain

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 300;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKVQTE 90
|||||
DB 187 DPKVQTE 193

RESULT 48
AD2900
succinyl-CoA synthetase alpha chain [imported] - Agrobacterium tumefaciens (strain C58,
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C/Accession: AD2900
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:11743193
A/Accession: AD2900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-300 <KUR>
A/Cross-references: GB:AE008688; PIDN:AAL43618.1; PID:g17741139; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: sucd
A/Map position: circular chromosome
C/Superfamily: succinate-CoA ligase (ADP-forming) alpha chain

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 300;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKVQTE 90
|||||
DB 187 DPKVQTE 193

RESULT 49
AF3269
succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) [imported] - Brucella melitensis (strain
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C/Accession: AF3269
R/DelVecchio, V.G.; Kapatal, V.; Redkar, R.U.; Patra, G.; Mujer, C.; Log, T.; Ivanova,
.; Mazur, M.; Goldeman, E.; Selkov, E.; Elzer, P.H.; Haglue, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A/Reference number: AD3252; PMID:11756688
A/Accession: AF3269
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-300 <KUR>
A/Cross-references: GB:AE008917; PIDN:AAL51321.1; PID:g17982017; GSPDB:GN00190
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME10139

```

A:Map position: 1
 C:Superfamily: succinate-CoA ligase (ADP-forming) alpha chain
 C:Keywords: acid-thiol ligase; coenzyme A

Query Match 0.7%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPVKGTE 90
 |||||
 Db 187 DPVKGTE 193

RESULT 50

dipeptide transport system permease protein dpqc - Escherichia coli (strain K-12)

C:Species: Escherichia coli
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
 C:Accession: S47764; S61433; A65153
 R:Plunkett, G.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: S47666

A:Accession: S47764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-300 <PLU>
 A:Cross-references: EMBL:U00039; NID:G466582; PIDN:AMB18520.1; PID:G466681
 R:Abouhamad, W.N.; Manson, M.D.
 Mol. Microbiol. 14, 1077-1092, 1994
 A:Title: The dipeptide permease of Escherichia coli closely resembles other bacterial tr
 A:Reference number: S61431; MUID:95231286; PMID:7556291
 A:Accession: S61433
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-300 <ABO>

A:Cross-references: EMBL:L08399; NID:G349224; PIDN:AAA23704.1; PID:G349227
 R:Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.U.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: A65153
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-300 <BLAT>

A:Cross-references: GB:AE000431; GB:U00096; NID:G1789957; PIDN:AAC76567.1; PID:G1789964;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: dpqc
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ALLTVL 926
 |||||
 Db 275 ALLTVL 281

RESULT 51

F91181
 dipeptide transport system permease protein 2 EC64422 [imported] - Escherichia coli (str

C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: F91181
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C.
 Gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A:Reference number: A39629; MUID:21156231; PMID:11258796
 A:Accession: F91181
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-300 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA837845.1; PID:G13363896; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD_0509952
 C:Genetics:
 A:Gene: EC64422
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ALLTVL 926
 |||||
 Db 275 ALLTVL 281

RESULT 52

B86028
 dipeptide transport system permease protein 2 [imported] - Escherichia coli (strain O157

C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: B86028
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; DiMantante, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B86028
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-300 <STO>
 A:Cross-references: GB:AE005174; NID:G12518266; PIDN:AAG58686.1; GSPDB:GN00145; UMGF:Z45
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: dpqc
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ALLTVL 926
 |||||
 Db 275 ALLTVL 281

RESULT 53

A10486
 dipeptide transport system permease protein dpqc [imported] - Yersinia pestis (strain CC

C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: A10486
 R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: A10486
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-300 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC93461.1; PID:G15981907; GSPDB:GN00175
 C:Genetics:
 A:Gene: dpqc
 C:Superfamily: oligopeptide permease protein oppb

Query Match 0.7%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ALLTVL 926

Db 275 AILLTVL 281

RESULT 54

AG0983

disputed transport system permease protein DPPC STY4170 [imported] - *Salmonella enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:Note: this species has also been called *Salmonella typhi*
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C/Accession: AG0983

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dord, L.; White, N.; Farrar, S.; Moul, S.; O'Garra, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AG0983

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1300 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07995.1; PID:g16504980; GSPDB:GN00176
C:Genetics:

A:Gene: STY4170
C:Superfamily: oligopeptide permease protein oppB

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 300;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AILLTVL 926
Db 275 AILLTVL 281

RESULT 55

E86591

CT580 hypothetical protein [imported] - *Chlamydia pneumoniae* (strain J138)
C:Species: *Chlamydia pneumoniae*
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001

C/Accession: E86591
R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000

A>Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
A:Reference number: A86491; PMID:10871362
A:Accession: E86591

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-303 <STO>
A:Cross-references: GB:BA000008; NID:g8979181; PIDN:BAA99015.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:

A:Gene: CPJ0807

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 303;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 SKLVNNA 948
Db 20 SKLVNNA 26

RESULT 56

D72031

CT580 hypothetical protein - *Chlamydia pneumoniae* (strain CWL029)
C:Species: *Chlamydia pneumoniae*
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000

C/Accession: D72031
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lämmler, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.

A:Reference number: A72000; PMID:99206606; PMID:10192388

A:Accession: D72031

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-303 <ARN>
A:Cross-references: GB:AB001662; GB:AE001363; NID:g4377118; PIDN:AAD18945.1; PID:g437711
A:Experimental source: strain CWL029
C:Genetics:

A:Gene: CPN0807

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 303;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 SKLVNNA 948
Db 20 SKLVNNA 26

RESULT 57

JC4347

uroporphyrin-III C-methyltransferase (EC 2.1.1.107) homolog - *Vibrio anguillarum*
N:Alternate names: hypothetical 34.8K protein
C:Species: *Vibrio anguillarum*
C>Date: 21-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 05-May-2000

C/Accession: JC4347
R:Milton, D.L.; Norqvist, A.; Wolf-Matz, H.
Gene 164, 95-100, 1995

A>Title: Sequence of a novel virulence-mediating gene, *virc*, from *Vibrio anguillarum*.
A:Reference number: JC4347; PMID:96060845; PMID:7590330
A:Accession: JC4347

A:Molecule type: DNA

A:Residues: 1-306 <MTL>
A:Cross-references: GB:U17054; NID:g576654; PIDN:AAA6984.1; PID:g576655
A:Experimental source: VAN20
C:Genetics:

A:Gene: *cysG*

C:Keywords: methyltransferase; S-adenosylmethionine; virulence

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 306;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 PVLVNTI 264
Db 134 PVLVNTI 140

RESULT 58

AB0078

lysr-family regulatory protein YPO0631 [imported] - *Yersinia pestis* (strain C092)
C:Species: *Yersinia pestis*
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C/Accession: AB0078
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davis, R.M.; Davies, P.; Dougan, G.;
H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001

A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB00001; PMID:21470413; PMID:11586360
A:Accession: AB0078

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-310 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89485.1; PID:g15978721; GSPDB:GN00175
C:Genetics:

A:Gene: YPO0631

C:Superfamily: conserved hypothetical protein H11364

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 310;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HLSARVR 15
 |||||
 Db 277 HLSARVR 283

RESULT 59

C97224
 hypothetical protein CAC2635 [imported] - Clostridium acetobutylicum
 C/Species: Clostridium acetobutylicum
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C/Accession: C97224
 R/Molling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: C97224
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-315 <KUR>
 A/Cross-references: GB:AE001437; PIDN:AAK80582.1; PID:G15025662; GSPDB:GN00168
 A/Experimental source: Clostridium acetobutylicum ATCC824
 C/Genetics:
 A/Gene: CAC2635

Query Match 0.7%; Score 7; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 KIYSINV 577
 |||||
 Db 306 KIYSINV 312

RESULT 60

J02217
 peroxidase (EC 1.11.1.7) precursor, anionic - Japanese aspen x large-toothed aspen
 C/Species: Populus sibirica x Populus grandidentata (Japanese aspen x large-toothed aspen)
 C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000
 C/Accession: J02217
 R/Kawai, S.; Matsumoto, Y.; Kajita, S.; Yamada, K.; Katayama, Y.; Morohoshi, N.
 Biosci. Biotechnol. Biochem. 57, 131-133, 1993
 A/Title: Nucleotide sequence for the genomic DNA encoding an anionic peroxidase gene from Japanese aspen
 A/Reference number: J02217; MUID:93163019; PMID:7764045
 A/Accession: J02217
 A/Molecule type: DNA
 A/Residues: 1-318 <KAW>
 A/Cross-references: GB:D11102; NID:G217996; PIDN:BA01877.1; PID:G217997
 C/Genetics:
 A/Introns: 68/3; 131/3; 186/1

C/Superfamily: peroxidase
 C/Keywords: chromoprotein, glycoprotein, heme, iron, metalloprotein, oxidoreductase
 F/1-21/Domains: signal sequence #status predicted <SIG>
 F/22-318/Product: peroxidase, anionic #status predicted <MAT>
 F/32-111/Disulfide bonds: #status predicted
 F/34-91,166,203,253/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/59/active site: Arg #status predicted
 F/63/188/Binding site: heme iron (His) (axial ligands) #status predicted
 F/65-70/Disulfide bonds: #status predicted
 F/117-314/Disulfide bonds: #status predicted
 F/195-223/Disulfide bonds: #status predicted

Query Match 0.7%; Score 7; DB 2; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLAGP 686
 |||||
 Db 129 VTLAGP 135

RESULT 61

S01774

stable inheritance 36K protein - plasmid NR1

C/Species: plasmid NR1
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999
 C/Accession: S01774
 R/Tabuchi, A.; Min, Y.N.; Kim, C.K.; Fan, Y.L.; Womble, D.D.; Rownd, R.H.
 J. Mol. Biol. 202, 511-525, 1988
 A/Title: Genetic organization and nucleotide sequence of the stability locus of IncFII
 A/Reference number: S01774; MUID:89011976; PMID:3172224
 A/Accession: S01774
 A/Molecule type: DNA
 A/Residues: 1-320 <TAB>
 A/Cross-references: EMBL:X12777; NID:943001; PIDN:CAA31264.1; PID:943002
 C/Genetics:
 A/Gene: stbA
 A/Gene: stbA
 A/Gene: plasmid

Query Match 0.7%; Score 7; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 FFKTNS 392
 |||||
 Db 301 FFKTNS 307

RESULT 62

A24920
 36K para protein - Escherichia coli plasmid R1
 C/Species: Escherichia coli
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
 C/Accession: A24920
 R/Gerdes, K.; Molin, S.
 J. Mol. Biol. 190, 269-279, 1986
 A/Title: Partitioning of plasmid R1. Structural and functional analysis of the para locus
 A/Reference number: A24920; MUID:87060986; PMID:3023637
 A/Accession: A24920
 A/Molecule type: DNA
 A/Residues: 1-320 <GER>
 C/Genetics:
 A/Gene: plasmid

Query Match 0.7%; Score 7; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 FFKTNS 392
 |||||
 Db 301 FFKTNS 307

RESULT 63

F82904
 conserved hypothetical U0330 [imported] - Ureaplasma urealyticum
 C/Species: Ureaplasma urealyticum
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: F82904
 R/Glaes, J.I.; Lefkowitz, E.J.; Glaes, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 Submitted to Genbank, February 2000
 A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
 A/Reference number: A82870
 A/Accession: F82904
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-327 <GLA>
 A/Cross-references: GB:AE002130; GB:AF222894; NID:G6899302; PIDN:AAF30739.1; GSPDB:GN001
 A/Experimental source: serovar 3, biovar 1
 C/Genetics:
 A/Gene: U0330
 A/Gene: code: SGC3

Query Match 0.7%; Score 7; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 FMILTLV 475
 |||||
 Db 170 FMILTLV 176

RESULT 64

A:Accession: A96997
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 R:Moiling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A96997
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-336 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78764.1; PID:g15023675; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 A:Gene: CAC0788

Query Match 0.7%; Score 7; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 921 ILTLVT 927
 |||||
 Db 19 ILTLVT 25

RESULT 65

S55491
 probable galactosyltransferase (EC 2.4.1.-) SPAC5H10.13c [similarity] - fission yeast (S
 C:Species: Schizosaccharomyces pombe
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
 C:Accession: T38977; S55491
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z21821
 A:Accession: T38977
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-346 <CO2>
 A:Cross-references: EMBL:Z49811; NID:9854599; PIDN:CAA89963.1; PID:9854612; GSPDB:GN0006
 A:Experimental source: strain 972h; cosmid C5H10
 C:Gene: SPAC5H10.13c
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces pombe alpha-1,2-galactosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 0.7%; Score 7; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 556 TTFHRS 562
 |||||
 Db 81 TTFHRS 87

RESULT 66

A:DECHP
 2-dehydro-3-deoxy-phosphonate aldolase (EC 4.1.2.15) (Phe-sensitive) - Escherichia
 N:Alternate names: phospho-2-dehydro-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyhe
 C:Species: Escherichia coli
 C:Date: 18-Aug-1982 #sequence_revision 17-Dec-1982 #text_change 03-Jun-2002
 C:Accession: A01106; B64811
 R: Davies, W.D.; Davidson, B.E.

Nucleic Acids Res. 10, 4045-4058, 1982
 A>Title: The nucleotide sequence of aroG, the gene for 3-deoxy-D-arabinohexulose-7
 A:Reference number: A01106; MUID:82274236; PMID:6125934
 A:Accession: A01106

A:Molecule type: DNA
 A:Residues: 1-350 <DAV>
 A:Cross-references: GB:U01591; NID:g145367; PIDN:AAA23492.1; PID:g145368
 A:Experimental source: strain K12
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B64811

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-350 <BLAT>

A:Cross-references: GB:AE000178; GB:U00096; NID:g1786967; PIDN:AACT3841.1; PID:g1786969

A:Experimental source: strain K-12, substrain MG1655

C:Gene: aroG

A:Map position: 17 min

C:Function:

A>Description: aldehyde-lyase; carbon-carbon lyase; this is one of the DAP synthases th

ic acid-7-phosphate

A:Pathway: aromatic amino acid biosynthesis; shikimate pathway

A>Note: the first reaction in aromatic amino acid biosynthesis

A>Note: feedback-inhibited by phenylalanine; the other two DAP synthases are tyrosine-

C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase

C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; shik

Query Match 0.7%; Score 7; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 AGEFLDM 103
 |||||
 Db 141 AGEFLDM 147

RESULT 67

AG0593
 phospho-2-dehydro-3-deoxyheptonate aldolase (DAP synthetase) phenylalanine repressible
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A>Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG0593
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Mowle, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AG0593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05217.1; PID:g16501987; GSPDB:GN00176
 C:Gene: SRY0801
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase

Query Match 0.7%; Score 7; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 AGEFLDM 103
 |||||
 Db 141 AGEFLDM 147

RESULT 68

F90726
 2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) [similarity]
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
 C:Accession: F90726
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 gaaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A9629; PMID:21156231; PMID:11258796
 A:Accession: F90726
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <NAV>
 A:Cross-references: GB:BA000007; PIDN:BAH34205.1; PID:g13360241; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: EC80782
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 0.7%; Score 7; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGEFLDM 103
 |||||
 DB 141 AGEFLDM 147

RESULT 69
 G85577
 2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) [similarity]
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002
 C:Accession: G85577
 R:Penna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 11ler, U.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Ayodada,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; PMID:21074935; PMID:11206551
 A:Accession: G85577
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <STO>
 A:Cross-references: GB:AE005174; NID:g12513683; PIDN:ANG55083.1; GSPDB:GN00145; UNCF:209
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: aroc
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 0.7%; Score 7; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGEFLDM 103
 |||||
 DB 141 AGEFLDM 147

RESULT 70
 A97788
 microcin C7 self-immunity protein homolog [imported] - Rickettsia conorii (strain Malish
 C:Species: Rickettsia conorii
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
 C:Accession: A97788
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc
 Science 293, 2033-2098, 2001
 A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A97700; PMID:21442074; PMID:11557893
 A:Accession: A97788
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-360 <RKR>
 A:Cross-references: GB:AE006914; PIDN:AAI02343.1; PID:g15619797; GSPDB:GN00173
 C:Genetics:
 A:Gene: mccF2

Query Match 0.7%; Score 7; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 GIKRTTY 880
 |||||
 DB 5 GIKRTTY 11

RESULT 71
 I64128
 2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) - Haemophilus
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
 C:Accession: I64128
 R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
 i; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, C.
 , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; PMID:95350630; PMID:7542800
 A:Accession: I64128
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-362 <TIGR>
 A:Cross-references: GB:U12830; GB:I42023; NID:g1574389; PIDN:AAZ3197.1; PID:g1574392; T
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase

Query Match 0.7%; Score 7; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGEFLDM 103
 |||||
 DB 148 AGEFLDM 154

RESULT 72
 F87100
 L-alanine dehydrogenase [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: F87100
 R:Coile, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
 R.; Davies, R.M.; Devlin, K.; Duthey, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; PMID:21128732; PMID:11234002
 A:Accession: F87100
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-371 <STO>
 A:Cross-references: GB:AL450380; NID:g13093357; PIDN:CAC30483.1; GSPDB:GN00147
 C:Genetics:
 A:Gene: ald
 C:Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

Query Match 0.7%; Score 7; DB 2; Length 371;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 DLGAVK 369
 |||||

Db 224 DLEGAVK 230

RESULT 73

T20093

hypothetical protein C50B6.10 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000

C/Accession: T20093

R/Percy, C.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19222

A/Accession: T20093

A/Status: preliminary; translated from GB/EMBL/DDBT

A/Molecule type: DNA

A/Residues: 1-371 <WTL>

A/Cross-references: EMBL:Z01050; PIDN:CAH02859.1; GSPDB:GN00023; CESP:C50B6.10

A/Experimental source: clone C50B6

C/Genetics:

A/Map position: 5

A/Intons: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein C45H4.12

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Length 371;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 VGVSRT 521

Db 360 VGVSRT 366

RESULT 74

A70791

probable anion transporting ATPase - *Mycobacterium tuberculosis* (strain H37RV)

C/Species: *Mycobacterium tuberculosis*

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C/Accession: A70791

R/Colo, S.T.; Brosch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Seares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

C/Accession: A70791

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-386 <COL>

A/Cross-references: GB:AL022121; GB:AL123456; NID:93261559; PIDN:CA118002.1; PID:el26454

A/Experimental source: strain H37RV

C/Genetics:

A/Map position: 5

A/Intons: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein C45H4.12

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 386;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 RLRLL 30

Db 178 RLRLL 184

RESULT 75

T12456

hypothetical protein DKF2p564M2423.1 - human

C/Species: *Homo sapiens* (man)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C/Accession: T12456

R/Mambuti, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A/Reference number: Z17524

A/Accession: T12456

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-387 <MAN>

A/Cross-references: EMBL:AL080119

A/Experimental source: fetal brain; clone DKF2p564M2423

C/Genetics:

A/Note: DKF2p564M2423.1

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 387;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 ADTENKE 493

Db 247 ADTENKE 253

RESULT 76

C82637

porphyrin biosynthesis protein Xfr1797 [imported] - *Xylella fastidiosa* (strain 945c)

C/Species: *Xylella fastidiosa*

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C/Accession: C82637

R/Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: C82637

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-389 <SIM>

A/Cross-references: GB:AE004001; GB:AE003849; NID:99106664; PIDN:AAF84605.1; GSPDB:GN001

A/Experimental source: strain 945c

R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carreir, D.M.; Carreir, H.

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincini, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Klatsjima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiz

chado, M.A.; Madalra, A.M.B.N.; Madeira, H.M.R.; Martins, M.V.; Martins, E.

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F.

A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tashiro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A/Reference number: A59328

A/Contents: annotation

C/Genetics:

A/Map position: 5

A/Intons: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein C45H4.12

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 389;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 LPPRGLL 994

Db 181 LPPRGLL 187

RESULT 77

G89822

hypothetical protein SA0507 [imported] - *Staphylococcus aureus* (strain N315)

C/Species: *Staphylococcus aureus*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C/Accession: G89822

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

ma, A.; Mizutani-U, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: G89822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:BA000018; PID:g13700440; PIDN:BAB41738.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0507

Query Match 0.7%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 TAILTV 925
DB 108 TAILTV 114

RESULT 78

AH0334
probable long-chain fatty acid transport protein fadL [imported] - Versinia pestis (stra
C:Species: Versinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AH0334
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001

A:Title: Genome sequence of Versinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-423 <KUR>
A:Cross-references: GB:AL590842; PIDN:CA92983.1; PID:g15980722; GSPDB:GN00175
C:Genetics:
A:Gene: fadL

C:Superfamily: long-chain fatty acid transport protein fadL

Query Match 0.7%; Score 7; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 KTVPGSL 830
DB 256 KTVPGSL 262

RESULT 79

A12187
histidinol dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: A12187
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriuch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Takata, S
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-431 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAB74755.1; PID:g17132150; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: hisD

C:Superfamily: histidinol dehydrogenase; histidinol dehydrogenase homology

Query Match 0.7%; Score 7; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HSHLSA 12
DB 61 HSHLSA 67

RESULT 80

H90131
regulator of epidermal growth factor receptor [imported] - Giardia theta nucleomorph
C:Species: nucleomorph Giardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H90131
R:Douglas, S.; Zanner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: H90131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-434 <DOU>
A:Cross-references: GB:AF083031; NID:g13794405; PIDN:AAK39782.1; GSPDB:GN00152
C:Genetics:
A:Gene: Ebi
A:Map position: 3
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 0.7%; Score 7; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 KNOXLEY 939
DB 304 KNOXLEY 310

RESULT 81

T36706
hypothetical protein SCH69.07c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36706
R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999

A:Reference number: Z21612
A:Accession: T36706
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-436 <MUR>
A:Cross-references: EMBL:AL079308; PIDN:CA845204.1; GSPDB:GN00070; SCOEDB:SCH69.07c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCH69.07c

Query Match 0.7%; Score 7; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 TVTLAGG 685
DB 187 TVTLAGG 193

RESULT 82

J01729
ankyrin-repeat protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: J01729
R:Zhang, H.; Schejter, D.C.; Fowle, W.H.; Goodman, H.M.
Plant Cell 4, 1575-1588, 1992
A:Title: Expression of antisense or sense RNA of an ankyrin repeat-containing gene block

A;Reference number: JQ1729; MUID:93104681; PMID:1281700
 A;Accession: JQ1729
 A;Molecule type: mRNA
 A;Residues: 1-439 <ZNA>
 A;Cross-references: GB:M82803; NID:g16743; PIDN:AAA32812.1; PID:g16744
 C;Genetics:
 A;Gene: AKR
 A;Intons: 262/1; 287/3; 320/3; 353/3; 386/3; 419/3
 C;Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology
 C;Keywords: cytoskeleton
 F;282-314/Domain: ankryrin repeat <RP1>
 F;315-347/Domain: ankryrin repeat <RP2>
 F;348-380/Domain: ankryrin repeat <RP3>
 F;381-413/Domain: ankryrin repeat <RP4>
 F;387-419/Domain: ankryrin repeat homology <AN1>

Query Match 0.7%; Score 7; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 SLIPGT 835
 DB 40 SLIPGT 46

RESULT 83
 A44751
 carotenoid-binding protein cbpa - *Synechococcus* sp.
 C;Species: *Synechococcus* sp.
 C;Date: 03-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
 C;Accession: A44751
 R;Reddy, K.J.; Masamoto, K.; Sherman, D.M.; Sherman, L.A.
 J. Bacteriol. 171, 3486-3493, 1989
 A;Title: DNA sequence and regulation of the gene (cbpa) encoding the 42-kilodalton cytop
 A;Reference number: A44751; MUID:89255122; PMID:2498292
 A;Accession: A44751
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-450 <RED>
 A;Cross-references: EMBL:M27055; NID:g154493; PIDN:AAA27303.1; PID:g154494
 A;Note: the authors translated the codon ATC for residue 119 as Met

Query Match 0.7%; Score 7; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 TAAGASD 466
 DB 47 TAAGASD 53

RESULT 84
 S45051
 tubulin alpha-B chain - *Neurospora crassa*
 C;Species: *Neurospora crassa*
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C;Accession: S45051
 R;Kornat, U.; Turián, G.
 submitted to the EMBL Data Library, May 1994
 A;Description: Two alpha-tubulin genes of *Neurospora crassa* encode divergent proteins.
 A;Reference number: S45050
 A;Accession: S45051
 A;Molecule type: mRNA
 A;Residues: 1-451 <MON>
 A;Cross-references: EMBL:X79404; NID:g495132; PIDN:CAA55941.1; PID:g495133
 C;Superfamily: tubulin.
 C;Keywords: microtubule

Query Match 0.7%; Score 7; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 964 MEGEDVE 970

DB 442 MEGEDVE 448

RESULT 85
 T47824
 hypothetical protein F24G16.270 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
 C;Accession: T47824
 R;D'Angelis, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24477
 A;Accession: T47824
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-451 <DNA>
 A;Cross-references: EMBL:AL138647
 A;Experimental source: cultivar Columbia; BAC clone F24G16
 C;Genetics:
 A;Map position: 3
 A;Intons: 284/3; 324/3; 363/3; 393/3; 429/3
 A;Note: F24G16.270
 C;Superfamily: *Arabidopsis thaliana* hypothetical protein F24G16.270

Query Match 0.7%; Score 7; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 SSGCNVR 327
 DB 210 SSGCNVR 216

RESULT 86
 AB1104
 DNA repair protein Sme homolog lmo023 [imported] - *Listeria monocytogenes* (strain EGD-e
 C;Species: *Listeria monocytogenes*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C;Accession: AB1104
 R;Glasner, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feibi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schliuter, T.; Simoes, N.; Tixeront, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund
 A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1104
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-457 <GLA>
 A;Cross-references: GB:NC 003210; PIDN:CAD00760.1; PID:g16409598; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo023
 C;Superfamily: DNA repair protein sme

Query Match 0.7%; Score 7; DB 2; Length 457;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 ECTATLM 178
 DB 195 ECTATLM 201

RESULT 87
 T33787
 hypothetical protein F52F10.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
 C;Accession: T33787

R:Graves, T.; Henkhaus, J.; Wohldmann, J.; Bauer, C.; Duckels, G.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans_gosmid F52F10.
A:Reference number: Z21410
A:Accession: T33787

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-471 <GRA>

A:Cross-references: EMBL:AF101316; PIDN:AC69232.1; GSPDB:GN00023; CESP:F52F10.2
A:Experimental source: strain Bristol N2; clone F52F10
C:Genetics:

A:Gene: CESP:F52F10.2
A:Map position: 5

A:Insertions: 39/1; 122/2; 203/1; 261/1; 308/2; 355/2; 448/3
C:superfamily: Caenorhabditis elegans hypothetical protein C25E10.3

Query Match 0.7%; Score 7; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 CDPKYS 317
Db 397 CDPKYS 403

RESULT 88

E84853

hypothetical protein At2g42400 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84853

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanham, S.E.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-473 <STO>
A:Cross-references: GB:AE002093; NID:94567312; PIDN:AAD33723.1; GSPDB:GN00139

C:Genetics:
A:Gene: At2g42400
A:Map position: 2

Query Match 0.7%; Score 7; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 782 AELFHE 788
Db 335 AELFHE 341

RESULT 89

A64472

carbamoyl-phosphate synthase, large chain (EC 6.3.-.-) - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A64472
R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbach, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1085-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: A64472
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-487 <BUL>
A:Cross-references: GB:U67577; GB:L77117; NID:91592013; PID:91592023; TIGR:MTJ378; PID:9

C:Genetics:
A:Map position: FOR1326866-1328329
A:Start codon: TTG
C:Superfamily: carbamoyl-phosphate synthase large chain; biotin carboxylase homology
C:Keywords: ligase
F:11-470/Domain: biotin carboxylase homology <BCH>

Query Match 0.7%; Score 7; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 689 TSKGLKY 695
Db 194 TSKGLKY 200

RESULT 90

AF1130

transcription regulator homolog lmo0445 [imported] - Listeria monocytogenes (strain EGD-
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AF1130
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Me
ok, C.; Schluteler, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1130
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-495 <GUA>
A:Cross-references: GB:NC_003210; PIDN:CAC98524.1; PID:916409822; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:

A:Gene: lmo0445
A:Map position: 2

Query Match 0.7%; Score 7; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 ENKEVAR 496
Db 278 ENKEVAR 284

RESULT 91

T01937

hypothetical protein F1104.7 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999

C:Accession: T01937
R:Abu-Threideh, J.; Stoneking, T.; Langston, Y.; Trevasakis, E.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana F1104.

A:Reference number: Z14466
A:Accession: T01937
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-508 <ABU>
A:Cross-references: EMBL:AF096370; NID:93695372; PID:93695380

A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: F1104.7

Query Match 0.7%; Score 7; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 364 LEGAVKL 370

Db 445 LEGAVKL 451

RESULT 92

penton base protein - fowl adenovirus 1
S52321
N/Alternate names: envelope protein
C/Species: Aviadnavovirus gall (fowl adenovirus 1, CEL0)
C/Date: 08-May-1995 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
C/Accession: S52321
R/Akopian, T.A.; Lazareva, S.E.; Tikhomirov, E.E.; Karpov, V.A.; Naroditsky, B.S.
submitted to the EMBL Data Library, February 1995
A/Description: Genes for Avian adenovirus CEL0 penton base and core polypeptides.
A/Reference number: S52320
A/Accession: S52321
A/Molecule type: DNA
A/Residues: 1-515 <AKO>
A/Cross-references: EMBL:Z48167; NID:9755698; PIDN:CAA88181.1; PID:9663165
C/Superfamily: adenovirus penton protein
C/Keywords: envelope protein

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 515;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 DLRIPEG 726

Db 181 DLRIPEG 187

RESULT 93

JE0335
nucleolar protein - human
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: JE0335
R/Ueki, N.; Kondo, M.; Seki, N.; Yano, K.; Oda, T.; Maehuo, Y.; Muramatsu, M.
Biochem. Biophys. Res. Commun. 252: 97-102, 1998
A/Title: NOLP: Identification of a novel human nucleolar protein and determination of se
A/Reference number: JE0335; MUID:99032811; PMID:9813152
A/Accession: JE0335
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-524 <UEK>
A/Cross-references: DDBJ:AB017800; NID:93892915; PIDN:BAA34576.1; PID:93892916

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 524;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 DDSAAS 150

Db 144 DDSAAS 150

RESULT 94

TS1836
high affinity nitrate transporter protein 2 ACNRT2-1 [similarity] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: T51836
R/Fillier, S.; Daniel-Vedele, F.
Planta 207: 461-469, 1999
A/Title: Expression analysis of a high affinity nitrate transporter from Arabidopsis the
A/Reference number: 225479; MUID:99136914; PMID:9951738
A/Accession: T51836
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-530 <FIL>
A/Cross-references: EMBL:AF093754; PIDN:AAC61170.1
C/Keywords: DNA binding; zinc finger
C/Genetics: ;

A/Map position: 1
C/Superfamily: nitrate transporter component
C/Keywords: nitrate transport

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 530;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKVGT 90

Db 474 DPKVGT 480

RESULT 95

B89771
hypothetical protein lcp (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: B89771
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogund
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357: 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: B89758; MUID:21311952; PMID:11418146

A/Accession: B89771

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-530 <KUR>

A/Cross-references: GB:BA000018; PID:913700026; PIDN:BA841325.1; GSPDB:GN00149

A/Experimental source: strain N315

C/Genetics: lcp

C/Superfamily: L-lactate permease

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 530;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 TAILLTV 925

Db 358 TAILLTV 364

RESULT 96

A31760
Ro/SS-A complex, 60K ribonucleoprotein - human
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Oct-1999
C/Accession: A31760; A30596
R/Deutscher, S.L.; Harley, J.B.; Keene, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85: 9479-9483, 1988
A/Title: Molecular analysis of the 60-kDa human Ro ribonucleoprotein.
A/Reference number: A31760; MUID:89071722; PMID:3200833
A/Accession: A31760
A/Molecule type: mRNA
A/Residues: 1-538 <DEU>
A/Cross-references: GB:U04137; NID:9177782; PIDN:AAA35493.1; PID:9177783
R/Ben-Cherif, E.; Gandy, B.J.; Tan, E.M.; Sullivan, K.F.
J. Clin. Invest. 83: 1284-1292, 1989
A/Title: Isolation and characterization of a cDNA clone encoding the 60-kD component of
A/Reference number: A30596; MUID:8918084; PMID:2649513
A/Accession: A30596
A/Molecule type: mRNA
A/Residues: 1-238; 'R', 240-292, 'DV', 295-300, 'A', 302-514, 'ALQNTLNKSR' <BEN>
A/Cross-references: GB:M25077; NID:9387656
A/Note: the sequence is revised in GenBank entry HUMANTANP, release 111.0, (PID:9387656)
C/Genetics: GDB:SSA2
A/Map position: 1931-1931
C/Keywords: DNA binding; zinc finger
F:305-323/Region: zinc finger CCH motif

Query Match 0.7%; Score 7; DB 2; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 VTIDMTL 775
 |||||
 DB 424 VTIDMTL 430

RESULT 97
 T36704
 probable dehydrogenase - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T36704
 R/Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A/Reference number: Z21612
 A/Accession: T36704
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-563 <MUR>
 A/Cross-references: EMBL:AL079308; PIDN:CAB45202.1; GSPDB:GN00070; SCOEDB:SCH69.05
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SCH69.05

Query Match 0.7%; Score 7; DB 2; Length 563;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 AYTSECF 276
 |||||
 DB 451 AYTSECF 457

RESULT 98
 A30098
 developmental protein xlgv7 - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Feb-1997
 C/Accession: A30098
 R/Miller, M.; Kloc, M.; Reddy, B.; Eastman, E.; Dreyer, C.; Eskin, L.
 Genes Dev. 3, 572-583, 1989
 A/Title: xlgv7: a maternal gene product localized in nuclei of the central nervous system
 A/Reference number: A30098; MUID:89252831; PMID:2721962
 A/Accession: A30098
 A/Molecule type: mRNA
 A/Residues: 1-591 <MIL>
 A/Cross-references: EMBL:J04494
 C/Keywords: DNA binding

Query Match 0.7%; Score 7; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 COAVIIP 745
 |||||
 DB 509 COAVIIP 515

RESULT 99
 T38920
 methyltetrahydrofolate reductase 2 - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T38920
 R/Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A/Reference number: Z21817
 A/Accession: T38920
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-603 <PEA>
 A/Cross-references: EMBL:Z69728; PIDN:CAA93581.1; GSPDB:GN00066; SPDB:SPAC56F8.10
 A/Experimental source: strain 972h-; cosmid c56F8
 C/Genetics:
 A/Gene: SPDB:SPAC56F8.10
 A/Map position: 1

Query Match 0.7%; Score 7; DB 2; Length 603;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 WDELPHG 133
 |||||
 DB 342 WDELPHG 348

RESULT 100
 T38908
 probable gamma-glutamyltransferase (EC 2.3.2.2) SPAC56E4.06c, precursor [similarity] -
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
 C/Accession: T38908
 R/Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, September 1997
 A/Reference number: Z21813
 A/Accession: T38908
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-611 <CON>
 A/Cross-references: EMBL:Z99261; PIDN:CAB16397.1; GSPDB:GN00066; SPDB:SPAC56E4.06c
 A/Experimental source: strain 972h-; cosmid c56E4
 C/Genetics:
 A/Gene: SPDB:SPAC56E4.06c
 A/Map position: 1
 C/Superfamily: gamma-glutamyltransferase
 C/Keywords: aminoacyltransferase

Query Match 0.7%; Score 7; DB 2; Length 611;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 ESGFSKS 733
 |||||
 DB 555 ESGFSKS 561

Search completed: April 22, 2003, 15:36:05
 Job time : 50 secs

